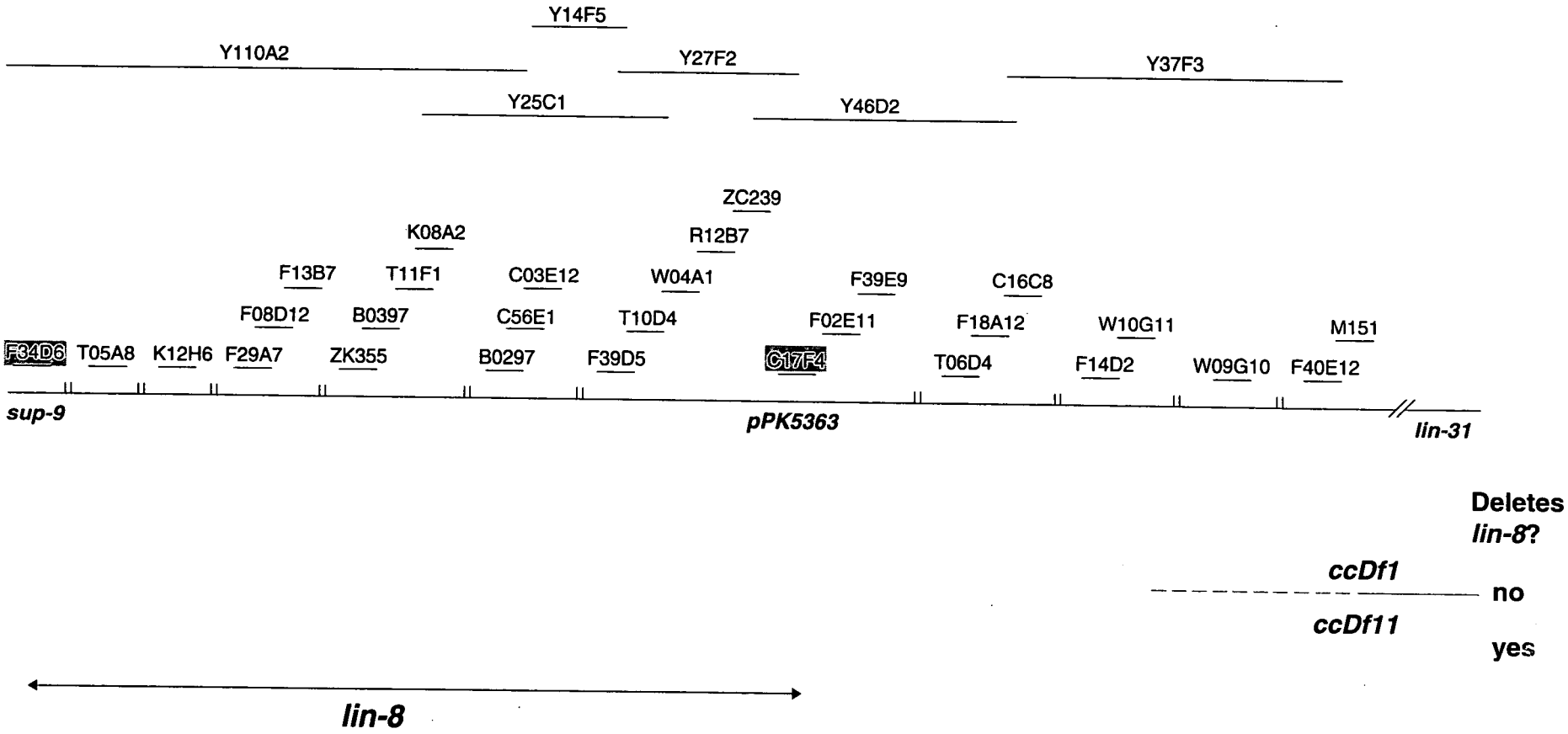
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Y25C1
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ZC239
K08A2
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F13B7
T11F1
C03E12
W04A1
F39E9
C16C8
F08D12
B0397
C56E1
T10D4
F02E11
F18A12
W10G11
M151
F84D6
T05A8
K12H6
F29A7
ZK355
B0297
F39D5
C17F4
T06D4
F14D2
W09G10
F40E12
sup-9
pPK5363
lin-31
Deletes lin-8?
ccDf1
no
ccDf11
yes
lin-8

Figure 1

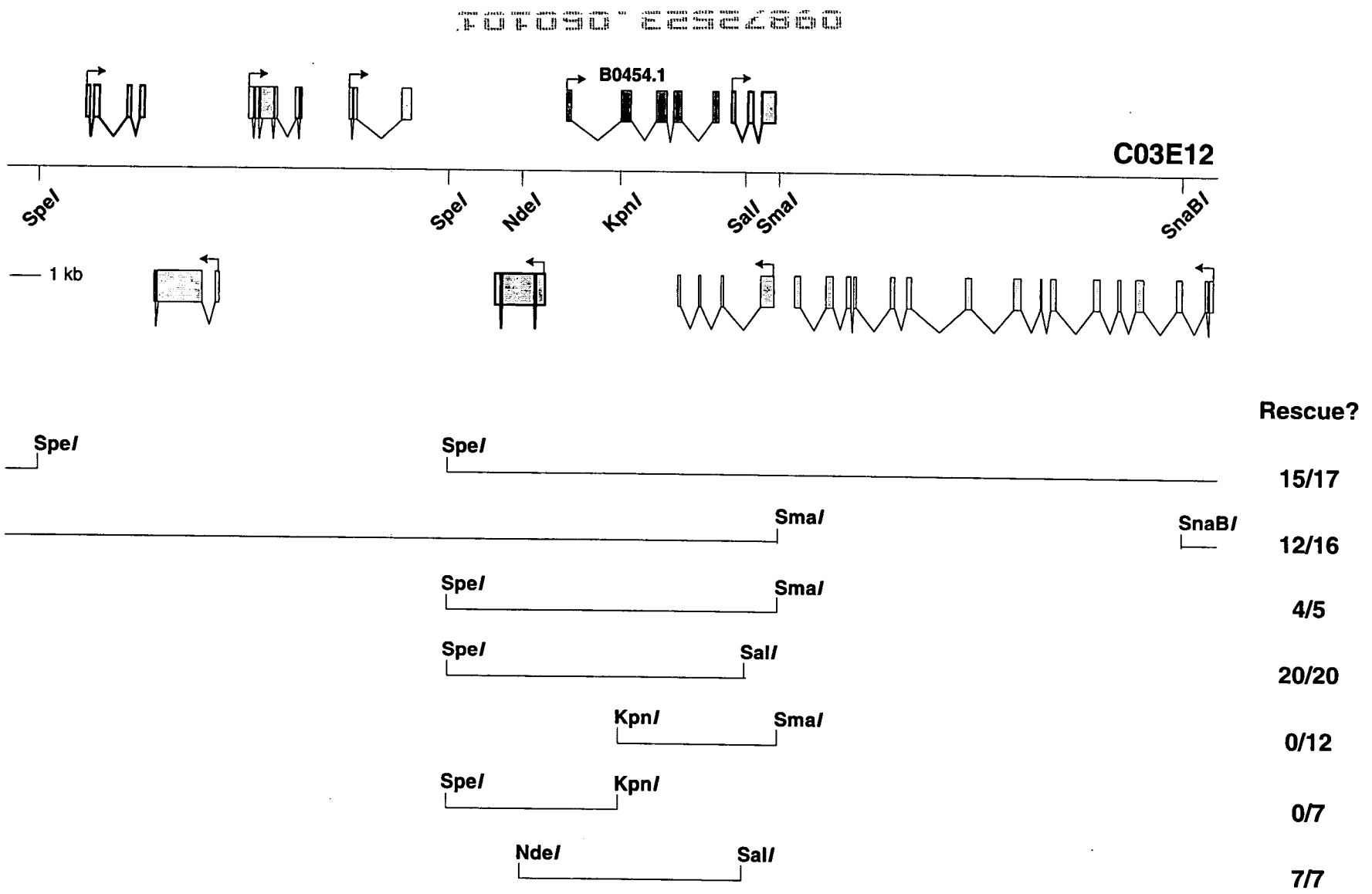
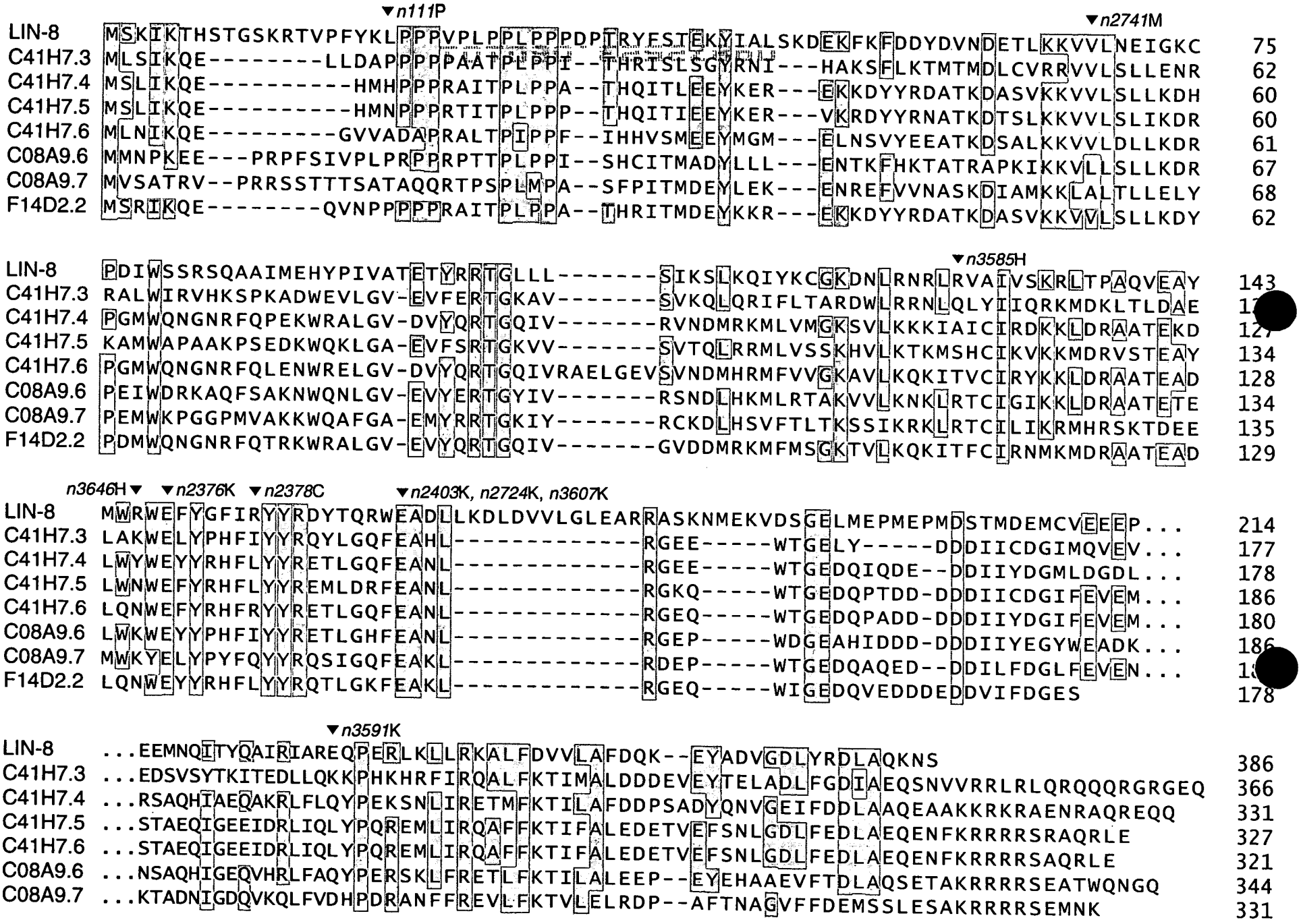

B0454.1
C03E12
SpeI
SpeI
NdeI
KpnI
SalI
SmaI
SnaBI
1 kb
Rescue?
SpeI
SpeI
15/17
SmaI
SnaBI
12/16
SpeI
SmaI
4/5
SpeI
SalI
20/20
KpnI
SmaI
0/12
SpeI
KpnI
0/7
NdeI
SalI
7/7

Figure 2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▼n2741M
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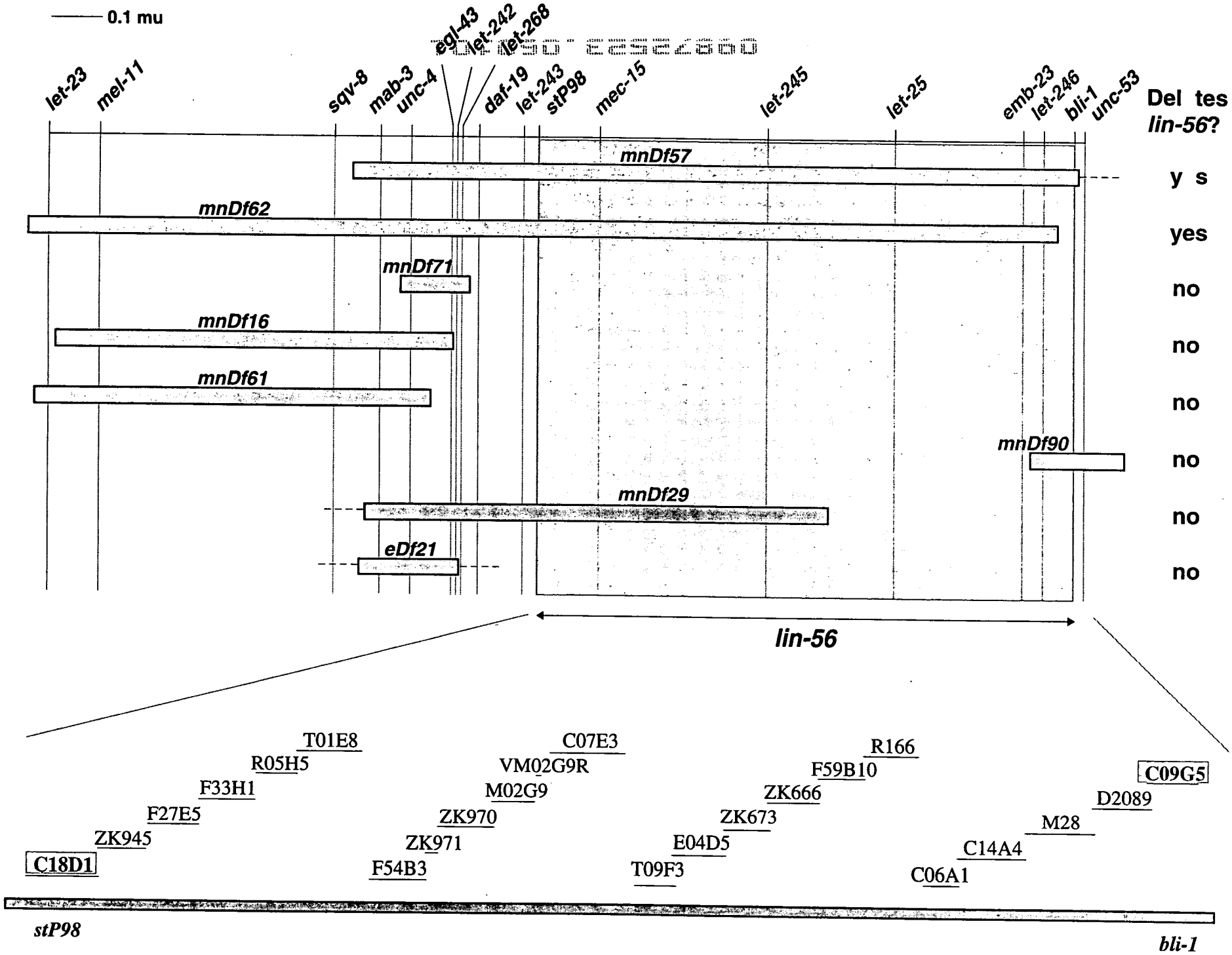
C41H7.3 MLSIKQE--------LLDAPPPPPAATPLPPI--THRISLSGYRNI---HAKSFLKTMTMDLCVRRVVLSLLENR 62
C41H7.4 MSLIKQE----------HMHPPPRAITPLPPA--THQITLEEYKER---EKKDYYRDATKDASVKKVVLSLLKDH 60
C41H7.5 MSLIKQE----------HMNPPPRTITPLPPP--THQITIEEYKER---VKRDYYRNATKDTSLKKVVLSLIKDR 60
C41H7.6 MLNIKQE---------GVVADAPRALTPIPPF--IHHVSMEEYMGM---ELNSVYEEATKDSALKKVVLDLLKDR 61
C08A9.6 MMNPKEE---PRPFSIVPLPRPPRPTTPLPPI--SHCITMADYLLL---ENTKFHKTATRAPKIKKVLLSLLKDR 67
C08A9.7 MVSATRV--PRRSSTTTSATAQQRTPSPLMPA--SFPITMDEYLEK---ENREFVVNASKDIAMKKLALTLLELY 68
F14D2.2 MSRIKQE--------QVNPPPPPRAITPLPPA--THRITMDEYKKR---EKKDYYRDATKDASVKKVVLSLLKDY 62
▼n3585H
LIN-8 PDIWSSRSQAAIMEHYPIVATETYRRTGLLL-------SIKSLKQIYKCGKDNLRNRLRVAIVSKRLTPAQVEAY 143
C41H7.3 RALWIRVHKSPKADWEVLGV-EVFERTGKAV-------SVKQLQRIFLTARDWLRRNLQLYIIQRKMDKLTLDAE 1
C41H7.4 PGMWQNGNRFQPEKWRALGV-DVYQRTGQIV-------RVNDMRKMLVMGKSVLKKKIAICIRDKKLDRAATEKD 12
C41H7.5 KAMWAPAAKPSEDKWQKLGA-EVFSRTGKVV-------SVTQLRRMLVSSKHVLKTKMSHCIKVKKMDRVSTEAY 134
C41H7.6 PGMWQNGNRFQLENWRELGV-DVYQRTGQIVRAELGEVSVNDMHRMFVVGKAVLKQKITVCIRYKKLDRAATEAD 128
C08A9.6 PEIWDRKAQFSAKNWQNLGV-EVYERTGYIV-------RSNDLHKMLRTAKVVLKNKLRTCIGIKKLDRAATETE 134
C08A9.7 PEMWKPGGPMVAKKWQAFGA-EMYRRTGKIY-------RCKDLHSVFTLTKSSIKRKLRTCILIKRMHRSKTDEE 135
F14D2.2 PDMWQNGNRFQTRKWRALGV-EVYQRTGQIV-------GVDDMRKMFMSGKTVLKQKITFCIRNMKMDRAATEAD 129
n3646H▼ ▼n2376K ▼n2378C ▼n2403K, n2724K, n3607K
LIN-8 MWRWEFYGFIRYYRDYTQRWEADLLKDLDVVLGLEARRASKNMEKVDSGELMEPMEPMDSTMDEMCVEEEP... 214
C41H7.3 LAKWELYPHFIYYRQYLGQFEAHL----------RGEE-----WTGELY-----DDDIICDGIMQVEV... 177
C41H7.4 LWYWEYYRHFLYYRETLGQFEANL----------RGEE-----WTGEDQIQDE--DDIIYDGMLDGDL... 178
C41H7.5 LWNWEFYRHFLYYREMLDRFEANL----------RGKQ-----WTGEDQPTDD-DDDIICDGIFEVEM... 186
C41H7.6 LQNWEFYRHFRYYRETLGQFEANL----------RGEQ-----WTGEDQPADD-DDDIIYDGIFEVEM... 180
C08A9.6 LWKWEYYPHFIYYRETLGHFEANL----------RGEP-----WDGEAHIDDD-DDDIIYEGYWEADK... 186
C08A9.7 MWKYELYPYFQYYRQSIGQFEAKL----------RDEP-----WTGEDQAQED--DDILFDGLFEVEN... 1
F14D2.2 LQNWEYYRHFLYYRQTLGKFEAKL----------RGEQ-----WIGEDQVEDDDEDDVIFDGES 178
▼n3591K
LIN-8 ...EEMNQITYQAIRIAREQPERLKLLRKALFDVVLAFDQK--EYADVGDLYRDLAQKNS 386
C41H7.3 ...EDSVSYTKITEDLLQKKPHKHRFIRQALFKTIMALDDDEVEYTELADLFGDIAEQSNVVRRLRLQRQQQRGRGEQ 366
C41H7.4 ...RSAQHIAEQAKRLFLQYPEKSNLIRETMFKTILAFDDPSADYQNVGEIFDDLAAQEAAKKRKRAENRAQREQQ 331
C41H7.5 ...STAEQIGEEIDRLIQLYPQREMLIRQAFFKTIFALEDETVEFSNLGDLFEDLAEQENFKRRRRSRAQRLE 327
C41H7.6 ...STAEQIGEEIDRLIQLYPQREMLIRQAFFKTIFALEDETVEFSNLGDLFEDLAEQENFKRRRRSAQRLE 321
C08A9.6 ...NSAQHIGEQVHRLFAQYPERSKLFRETLFKTILALEEP--EYEHAAEVFTDLAQSETAKRRRRSEATWQNGQ 344
C08A9.7 ...KTADNIGDQVKQLFVDHPDRANFFREVLFKTVLELRDP--AFTNAGVFFDEMSSLESAKRRRRSEMNK 331

Figure 3


0.1 mu
egl-43
let-242
let-268
let-23
mel-11
sqv-8
mab-3
unc-4
daf-19
let-243
stP98
mec-15
let-245
let-25
emb-23
let-246
bli-1
unc-53
Del tes
lin-56?
mnDf57
y s
mnDf62
yes
mnDf71
no
mnDf16
no
mnDf61
no
mnDf90
no
mnDf29
no
eDf21
no
lin-56
T01E8
R05H5
F33H1
F27E5
ZK945
C18D1
C07E3
VM02G9R
M02G9
ZK970
ZK971
F54B3
R166
F59B10
ZK666
ZK673
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C06A1
stP98
bli-1
25 kb

Figure 4

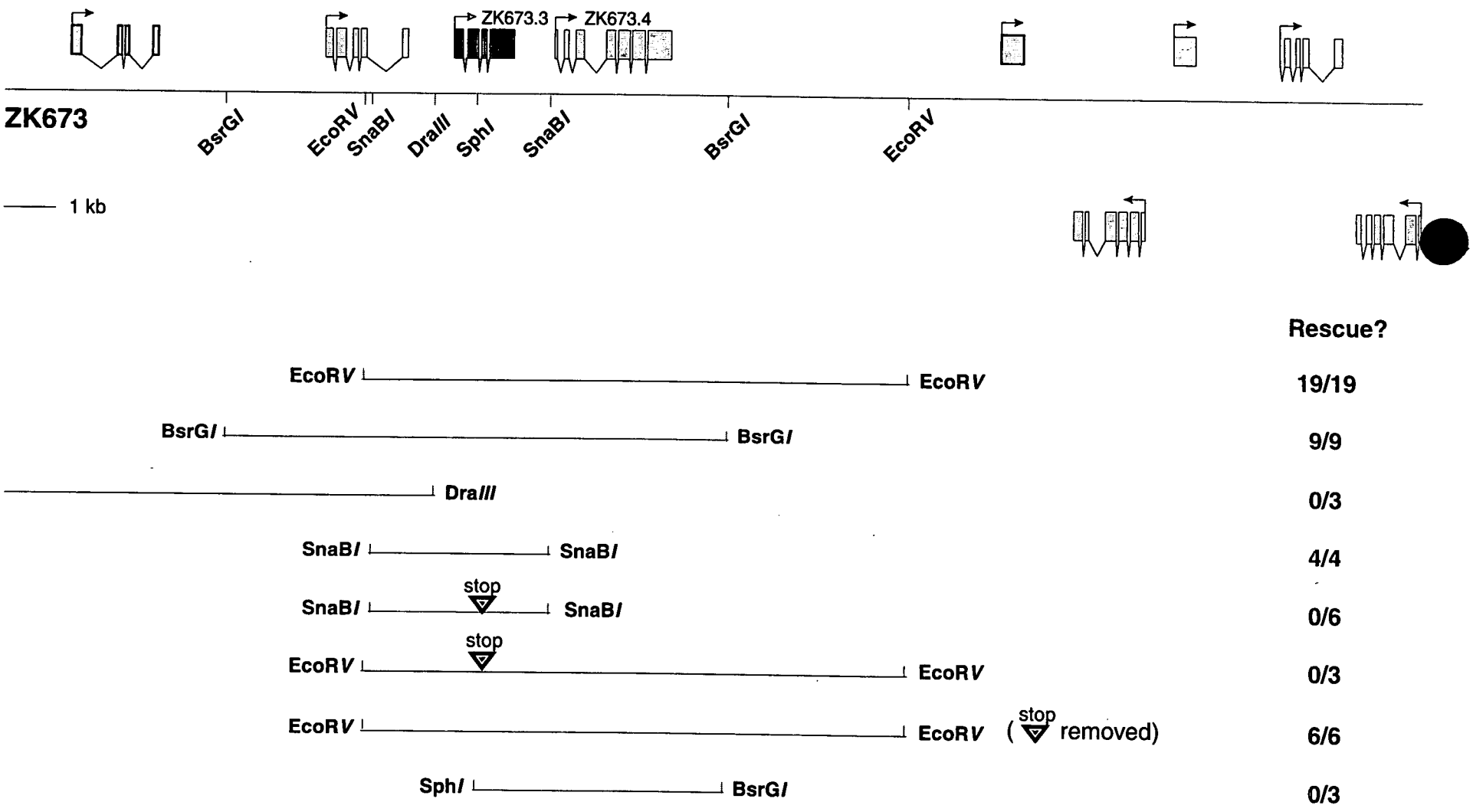

ZK673.3
ZK673.4
ZK673
BsrGI
EcoRV
SnaBI
DraIII
SphI
SnaBI
BsrGI
EcoRV
1 kb
Rescue?
EcoRV
EcoRV
19/19
BsrGI
BsrGI
9/9
DraIII
0/3
SnaBI
SnaBI
4/4
stop
SnaBI
SnaBI
0/6
stop
EcoRV
EcoRV
0/3
EcoRV
EcoRV
stop
removed)
6/6
SphI
BsrGI
0/3

Figure 5

```
LIN-56    MDHHAMYRTAEFNKTTVRLLAEFIEKTGQNATIVNMDSFLEFFAYLNPTA   50
          PIPTVPEIEKQLLLKSPIRCIVCGMETESDSAVTLSIDNASIILTATVIG  100
          YCRDPSDAVNQIRKESLRACTKHFNSIFHVIFEGLQIENTYCAHHAKYSL  150
          ANRWCKVYTMIRSSLGEQFTKFDVRNFKSILQSFLDTFGEIDDDKKDKES  200
          SHFDECFEEMDSENVEIKMESPQEEAAEKSKFSENLVEVKLEPIETHELD  250
          KTISDFSSSDIIDSSQKLQQNGFPEKVEQMDKYSNKLKDEASDKKYEKPG  300
          KKDYVEEEGYWAPITDSEDDEA                              322
```

```
LIN-56     69  RCIVCGMETESDSAVTLSIDNASIILTATVIGYCRDPSDAVNQIRKESLRACTKHFNSIF  128
LIN-15A   211  PCILCEKALLMRESIAMTDNEAVKVLMAAVMSGHFRMATAEKAIRHERLRMCYDHVDFVY  270
ZK673.4   176  PCIICGNEVPGHRSIRVSDDDAAIFLTAAVLTDQKTIRQAKRDILSEYLTVCLRHSLHYY  235
T25B9.8   274  PCLVCNQQMEMTKVRSVNNTDAYIMIYVCVMNDKYDMDKAKELARMQRFKCCVSHLDELY  333
                *  *                                               *  *
```

Figure 6

```
                                10        20        30        40
                         ....*....|....*....|....*....|....*....|
consensus             1 FDWEDYL---EETGARAAPVELF---DKQPVDSPPNGFKV 34
lin-61              146 VNYVNNCi-dGEIVGQTSLSPKF---DEGKALLSKHRFKV 181
lin-61               23 YLWESYLhqfEKGKTSFIPVEAF---NRNLTVNFNECVKE 59
lin-61              388 FRWDEYL---EKESAETLPLDLF---KPMPSQERLDKFKV 421
hl(3)mbt            206 WSWESYL---EEQKAITAPVSLFq--DSQAVTHNKNGFKL 240
hl(3)mbt            314 FSWSQYM---CSTRAQAAPKHMF---VSQSHSPPPLGFQV 347
hl(3)mbt            422 FCWEKYL---EETGASAVPTWAF-------KVRPPHSFLV 451
tumor sup(Dm)       819 FRWSEYLk--SKGKDVAAPIHLF----LNPFPISPNCFEI 852
tumor sup(Dm)       926 FSWSRYL---VKTGGKAAPRALFghlNMQQQMDVRNGFAV 962
tumor sup(Dm)      1035 FIWDDYI---SEVGGMAASKELF-------TPRQPMEYQE 1064
scmh1 (mouse)        28 FTWDKYL---KETCSVPAPVHCF----KQSYTPPSNEFKI 60
scml2 (human)       139 SSWPMFLl-kTLNGSEMASATLF---KKEPPKPPLNNFKV 174

                                50        60        70        80
                         ....*....|....*....|....*....|....*....|
consensus            35 -------GMKLEAVDP------RNPSLICVATVVEVKGYR 61
lin-61              182 -------GQRLELLNY------SNSTEIRVARIQEICGRR 208
lin-61               60 -------GVIFETVVHdydkncDSIQVRWFARIEKVCGYR 92
lin-61              422 iliskrvGLRLEAADM------CENQFICPATVKSVHGRL 455
hl(3)mbt            241 -------GMKLEGIDP------QHPSMYFILTVAEVCGYR 267
hl(3)mbt            348 -------GMKLEAVDR------MNPSLVCVASVTDVVDSR 374
hl(3)mbt            452 -------NMKLEAVDR------RNPALIRVASVEDVEDHR 478
tumor sup(Dm)       853 -------GMKLEAIDP------ENCSLFCVCSIVEVRGYR 879
tumor sup(Dm)       963 -------GMHLEAEDL------NDTGKICVATVTDILDER 989
tumor sup(Dm)      1065 -------RMKLEVVDQ------RNPCLIRPATVVTRKGYR 1091
scmh1 (mouse)        61 -------SMKLEAQDP------RNTTSTCIATVVGLTGAR 87
scml2 (human)       175 -------GMKLEAIDK------KNPYLICPATIGDVKGDE 201

                                90       100       110       120
                         ....*....|....*....|....*....|....*....|
consensus            62 LLLHFD----------GWDDR------YDFWCDADSPDIF 85
lin-61              209 MNVSITkkdfpeslpdADDDRqvfssgSQYWIDEGSFFIF 246
lin-61               93 VLAQFI----------GAD--------TKFWLNILSDDMF 114
lin-61              456 INVNFD----------GWDEE------FDELYDVDSHDIL 479
hl(3)mbt            268 LRLHFD----------GYSEC------HDFWVNANSPDIH 291
hl(3)mbt            375 FLVHFD----------NWDDT------YDYWCDPSSPYIH 398
hl(3)mbt            479 IKIHFD----------GWSHG------YDFWIDADHPDIH 502
tumor sup(Dm)       880 LKLSFD----------GYSSM------YDFWVNADSQDIF 903
tumor sup(Dm)       990 IRVHFD----------GWDDC------YDLWVHITSPYIH 1013
tumor sup(Dm)      1092 VQLHLD----------CWPTE------YYFWLEDDSPDLH 1115
scmh1 (mouse)        88 LRLRLD----------GSDNK------NDFWRLVDSSEIQ 111
scml2 (human)       202 VHITFD----------GWSGA------FDYWCKYDSRDIF 225

                               130
                         ....*....|....*
consensus            86 PVGWCEKNGHPLQPP 100
lin-61              249 PVGFAAVNGYQLNAK 263
lin-61              115 GLANAAM-SDPNMDK 128
lin-61              480 PIGWCEAHSYVLQPP 494
hl(3)mbt            292 PAGWFEKTGHKLQLP 306
hl(3)mbt            399 PVGWCQKQGKPLTPP 413
hl(3)mbt            503 PAGWCSKTGHPLQPP 517
tumor sup(Dm)       904 PPGWCDETARVLQAP 918
tumor sup(Dm)      1014 PCGWHEGRQQLIVPP 1028
tumor sup(Dm)      1116 PIGWCEATSHELETP 1130
scmh1 (mouse)       112 PIGNCEKNGGMLQPP 126
scml2 (human)       226 PAGWCRLTGDVLQPP 240
```

Figure 7

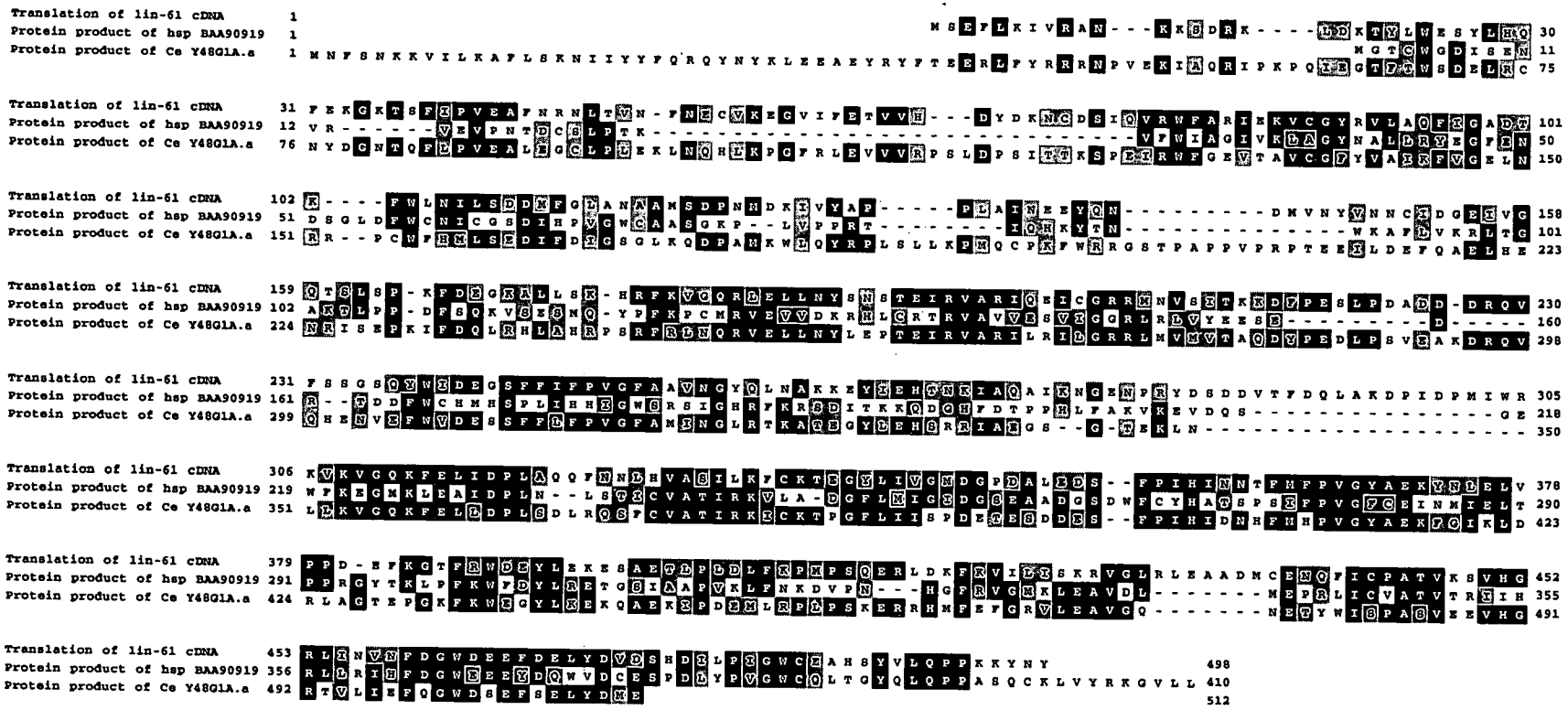
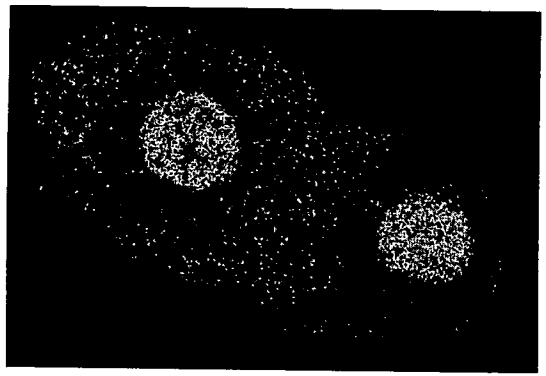

Translation of lin-61 cDNA
Protein product of hsp BAA90919
Protein product of Ce Y48G1A.a

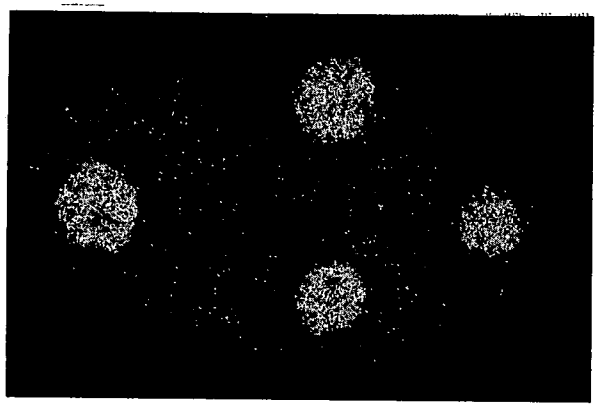
Figure 8

A



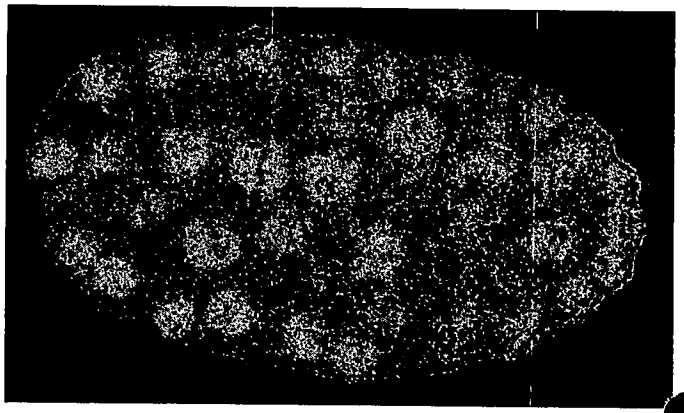
2-cell embryo

B



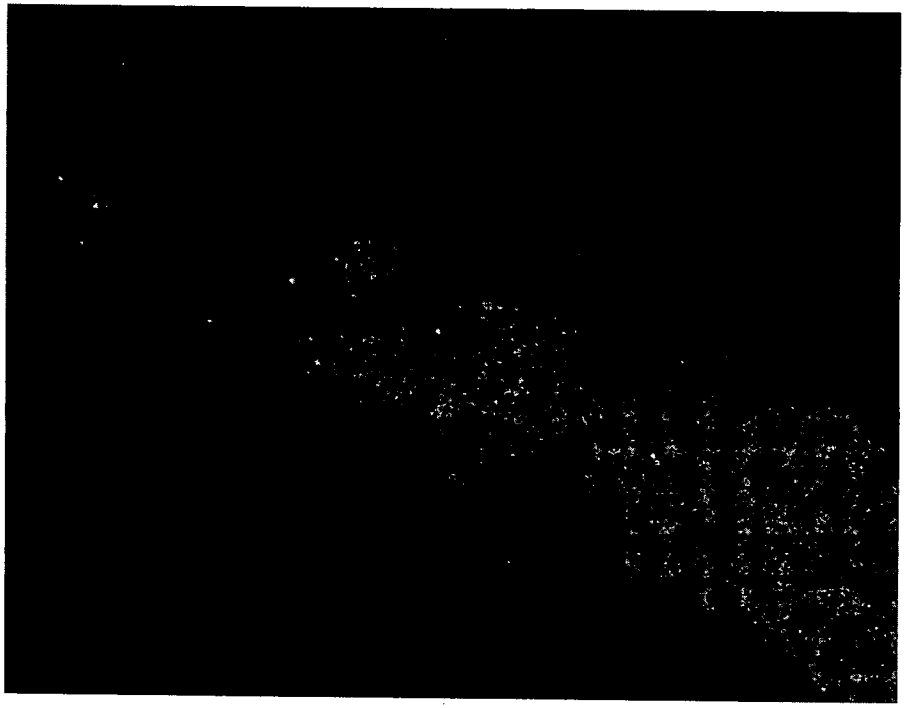
4-cell embryo

C



multicellular embryo

D



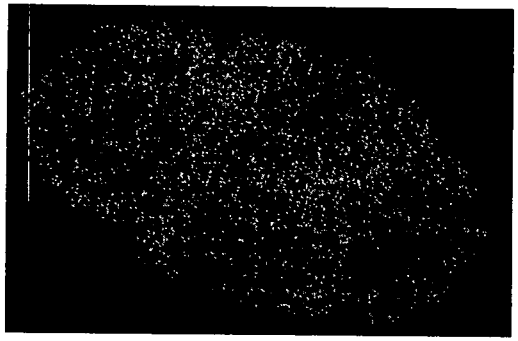
vulval region of an L4 larva

Figure 9

A

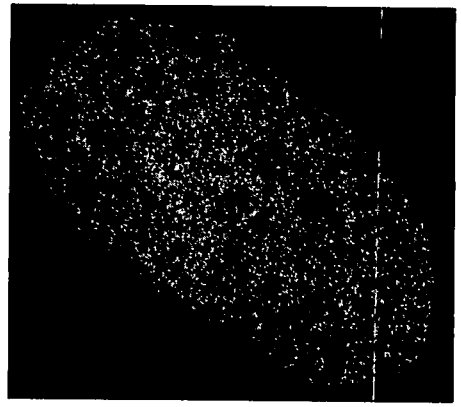
2-cell embryo

B



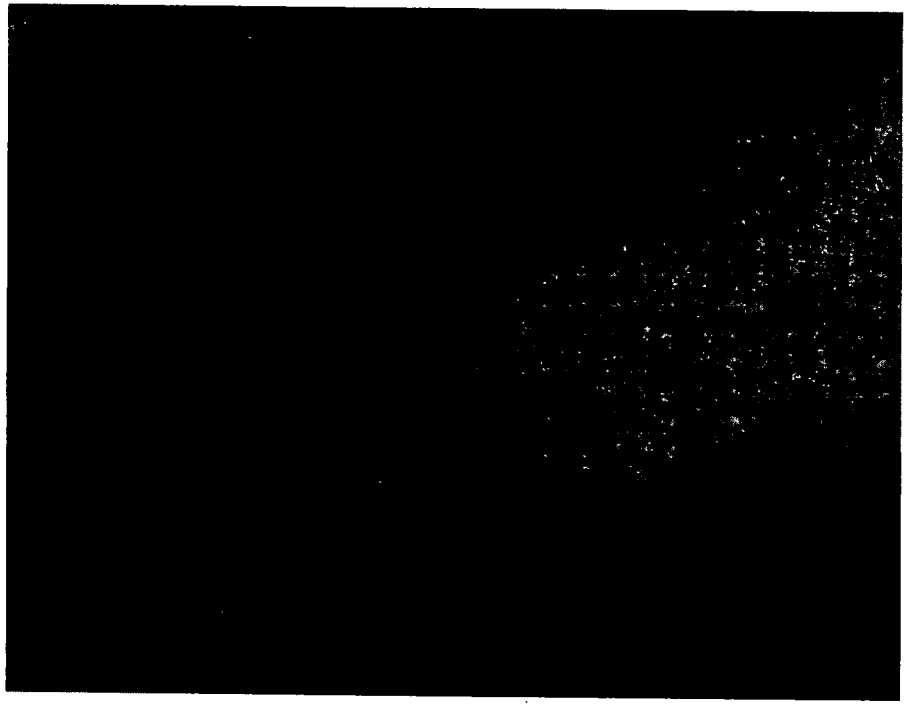
4-cell embryo

C



multicellular embryo

D



vulval region of an L4 larva

Figure 10

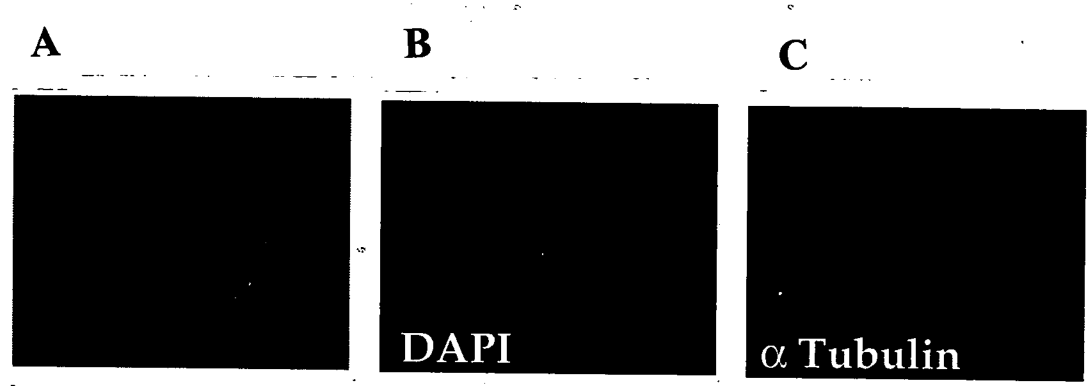


Figure 11

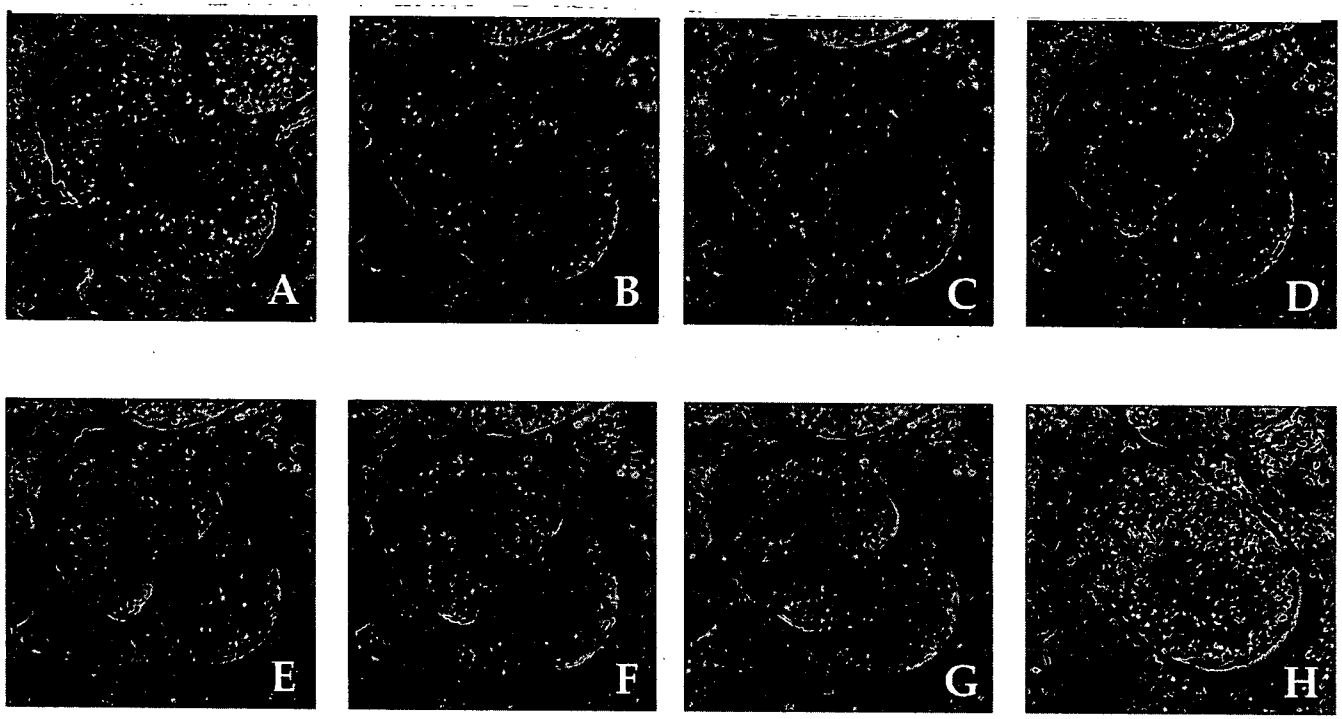


Figure 12

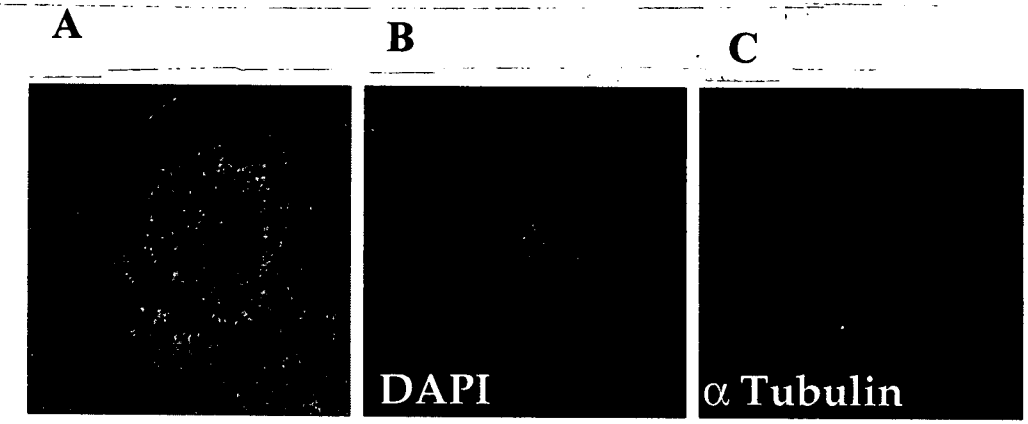


Figure 13